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File 143: Biol. & Agric. Index 1983-2002/May
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Set Items Description

Cost is in DialUnits

?ds

Set	Items	Description
S1	245	(VC167? OR (VC (2N) 167)) (100N) (CAMPYLOBACT? OR JEJUNI?)
S2	74	RD (unique items)
S3	17	S2/1998:2002
S4	57	S2 NOT S3

?t s4/9/3 4 5 6 8 9 10 11 12 13 14 17 18 19 20 21 22 26 27 31 32 33 34 56

4/9/3 (Item 3 from file: 155)
DIALOG(R) File 155: MEDLINE(R)

09391148 97290152 PMID: 9144908

Rapid and sensitive detection of **Campylobacter** spp. from chicken using the polymerase chain reaction.

Oyofo B A; Abd el Salam S M; Churilla A M; Wasfy M O
Research Science Department, Naval Medical Research Unit No. 3, Cairo, Egypt.

Zentralblatt fur Bakteriologie : international journal of medical microbiology (GERMANY) Apr 1997, 285 (4) p480-5, ISSN 0934-8840
Journal Code: 9203851

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

The polymerase chain reaction (PCR) using a target region in the flaA gene of *C. coli* VC167 flagellin was used to detect **Campylobacter** spp. in chicken without an enrichment culture. DNA extracted from 79 cloacal swabs from broiler chickens gave an amplification signal in the 450-bp region upon PCR. DNA extracted from 9 enteric and 6 non-enteric organisms included in the assay as negative controls failed to hybridize with the probe. Direct plating of all cloacal specimens on **Campylobacter** blood agar plates did not yield any growth. The PCR assay was sensitive enough to detect between 35-120 bacteria per PCR and thus provide a basis for detecting **Campylobacter** spp. in poultry.

Tags: Animal; Support, U.S. Gov't, Non-P.H.S.

Descriptors: *Campylobacter--isolation and purification--IP; *Chickens--microbiology--MI; *Polymerase Chain Reaction; Campylobacter--genetics--GE; Cloaca--microbiology--MI; DNA, Bacterial--analysis--AN; Flagellin--genetics--GE; Sensitivity and Specificity

CAS Registry No.: 0 (DNA, Bacterial); 12777-81-0 (Flagellin); 133606-66-3 (flaA protein)

Record Date Created: 19970710

4/9/4 (Item 4 from file: 155)
DIALOG(R) File 155: MEDLINE(R)

09200539 97101002 PMID: 8945529

Murine intranasal challenge model for the study of **Campylobacter** pathogenesis and immunity.

Baqar S; Bourgeois A L; Applebee L A; Mourad A S; Kleinovsky M T; Mohran Z; Murphy J R

Department of Infectious Diseases, Naval Medical Research Institute, Bethesda, Maryland 20889-5607, USA. baqar@mail2.nmri.nmrc.navy.mil

Infection and immunity (UNITED STATES) Dec 1996, 64 (12) p4933-9, ISSN 0019-9567 Journal Code: 0246127

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Campylobacter jejuni infection of mice initiated by intranasal administration was investigated as a potential model for studies of pathogenesis and immunity. By using a standard challenge (5×10^9 CFU), *C. jejuni* 81-176 was more virulent for BALB/c (72% mortality) than for C3H/Hej (50%), CBA/CAJ (30%), or C58/J (0%). Intranasal challenge of BALB/c was used to compare the relative virulence of three reference strains; *C. jejuni* 81-176 was more virulent (killing 83% of challenged mice) than *C. jejuni* HC (0%) or *C. coli* VC - 167 (0%). The course of intranasally initiated *C. jejuni* 81-176 infection in BALB/c was determined. *C. jejuni* was recovered from the lungs, intestinal tract, liver, and spleen at 4 h after challenge, the first interval evaluated. After this initial interval, three distinct patterns of infection were recognized: (i) a progressive decline in number of *C. jejuni* CFU (stomach, blood, lungs), (ii) decline followed by a second peak in the number of organisms recovered at 2 or 3 days postchallenge (intestine, liver, mesenteric lymph nodes), and (iii) persistence of approximately the same number of *C. jejuni* CFU during the course of the experiment (spleen). Intranasally induced infection initiated with a sublethal number of bacteria or intranasal immunization with killed *Campylobacter* preparations resulted in both the generation of *Campylobacter* antigen-specific immune responses and an acquired resistance to homologous rechallenge. The model was used to evaluate the relative virulence of nine low-in vitro-passage (no more than five passages) isolates of *C. jejuni* species from patients with diarrhea. The patient isolates were differentially virulent for mice; one killed all exposed mice, three were avirulent (no deaths) and the remainder showed an intermediate virulence, killing 17 to 33%. Mouse virulence of *Campylobacter* strains showed a trend toward isolates originating from individuals with watery diarrhea; however, no association was found between mouse virulence and other signs or symptoms. There were no observed relationships between mouse virulence and bacterial Lior serotype or Fla polymorphic group. Intranasal challenge of BALB/c with *C. jejuni* is a useful model for the study of infection and vaccination-acquired immunity to this agent.

Tags: Animal; Support, U.S. Gov't, Non-P.H.S.

Descriptors: **Campylobacter* Infections; **Campylobacter* *jejuni*; *Campylobacter* Infections--immunology--IM; *Campylobacter* Infections --physiopathology--PP; *Campylobacter* *jejuni*--pathogenicity--PY; Disease Models, Animal; Mice; Mice, Inbred BALB C; Mice, Inbred C3H; Mice, Inbred CBA; Virulence

Record Date Created: 19970108

4/9/5 (Item 5 from file: 155)
DIALOG(R) File 155: MEDLINE(R)

09061273 96423181 PMID: 8825782

Characterization of a post-translational modification of *Campylobacter* flagellin: identification of a sero-specific glycosyl moiety.

Doig P; Kinsella N; Guerry P; Trust T J

Department of Biochemistry and Microbiology, University of Victoria, British Columbia, Canada.

Molecular microbiology (ENGLAND) Jan 1996, 19 (2) p379-87, ISSN 0950-382X Journal Code: 8712028

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

The flagellins of *Campylobacter* spp. differ antigenically. In variants of *C. coli* strain VC167, two antigenic flagellin types determined by sero-specific antibodies have been described (termed T1 and T2). Post-translational modification has been suggested to be responsible for T1 and T2 epitopes, and, using mild periodate treatment and biotin hydrazide

labelling, flagellin from both VC167 -T1 and T2 were shown to be glycosylated. Glycosylation was also shown to be present on other *Campylobacter* flagellins. The ability to label all *Campylobacter* flagellins examined with the lectin LFA demonstrated the presence of a terminal sialic acid moiety. Furthermore, mild periodate treatment of the flagellins of VC167 eliminated reactivity with T1 and T2 specific antibodies LAH1 and LAH2, respectively, and LFA could also compete with LAH1 and LAH2 antibodies for binding to their respective flagellins. These data implicate terminal sialic acid as part of the LAH strain-specific epitopes. However, using mutants in genes affecting LAH serorecognition of flagellin it was demonstrated that sialic acid alone is not the LAH epitope. Rather, the epitope(s) is complex, probably involving multiple glycosyl and/or amino acid residues.

Tags: Support, Non-U.S. Gov't; Support, U.S. Gov't, Non-P.H.S.

Descriptors: *Campylobacter coli--metabolism--ME; *Campylobacter fetus --metabolism--ME; *Campylobacter jejuni--metabolism--ME; *Flagellin --metabolism--ME; Campylobacter coli--chemistry--CH; Campylobacter fetus --chemistry--CH; Campylobacter jejuni--chemistry--CH; Flagellin--chemistry --CH; Glycosylation; Mutation; Phenotype; Protein Processing, Post-Translational; Sialic Acids--metabolism--ME

CAS Registry No.: 0 (Sialic Acids); 12777-81-0 (Flagellin)

Record Date Created: 19961205

4/9/6 (Item 6 from file: 155)
DIALOG(R) File 155: MEDLINE(R)

09061272 96423180 PMID: 8825781

Identification and characterization of genes required for post-translational modification of *Campylobacter coli* VC167 flagellin.

Guerry P; Doig P; Alm R A; Burr D H; Kinsella N; Trust T J

Enteric Diseases Program, Naval Medical Research Institute, Bethesda, Maryland 20889, USA. guerry p@mail2.nmri.nnmrc.navy.mil

Molecular microbiology (ENGLAND) Jan 1996, 19 (2) p369-78, ISSN 0950-382X Journal Code: 8712028

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Two genes have been identified in *Campylobacter coli* VC167 which are required for the biosynthesis of post-translational modifications on flagellin proteins. The ptmA gene encodes a protein of predicted M(r) 28,486 which shows significant homology to a family of alcohol dehydrogenases from a variety of bacteria. The ptmB gene encodes a protein of predicted M(r) 26,598 with significant homology to CMP-N-acetylneuraminic acid synthetase enzymes involved in sialic acid capsular biosynthesis in *Neisseria meningitidis* and *Escherichia coli* K1. Site-specific mutation of either ptmA or ptmB caused loss of reactivity with antisera specific to the post-translational modifications and a change in the isoelectric focusing fingerprints relative to the parent strains. Mutation of ptmB, but not of ptmA, caused a change in apparent M(r) of the flagellin subunit in SDS-PAGE gels. The ptmA and ptmB genes are present in other strains of *Campylobacter*. In a rabbit model the ptmA mutant showed a reduced ability to elicit protection against subsequent challenge with heterologous strains of the same Lior serotype compared to the parental wild-type strain. This suggests that the surface-exposed post-translational modifications may play a significant role in the protective immune response.

Tags: Animal; Support, Non-U.S. Gov't; Support, U.S. Gov't, Non-P.H.S.

Descriptors: *Campylobacter coli--genetics--GE; *Flagellin--metabolism --ME; *Genes, Bacterial--genetics--GE; Amino Acid Sequence; Antibody Specificity; Base Sequence; Campylobacter--genetics--GE; Chromosome Mapping; Cloning, Molecular; Cytidine Monophosphate N-Acetylneuraminic Acid; DNA, Bacterial--genetics--GE; Molecular Sequence Data; Mutation; Protein Processing, Post-Translational; Rabbits; Sequence Analysis; Sequence Homology, Amino Acid

Molecular Sequence Databank No.: GENBANK/U25992
CAS Registry No.: 0 (DNA, Bacterial); 12777-81-0 (Flagellin);
3063-71-6 (Cytidine Monophosphate N-Acetylneuraminic Acid)
Record Date Created: 19961205

4/9/8 (Item 8 from file: 155)
DIALOG(R) File 155: MEDLINE(R)

08123810 94252999 PMID: 7515043

Structural and antigenic characteristics of *Campylobacter coli* FlaA flagellin.

Power M E; Guerry P; McCubbin W D; Kay C M; Trust T J
Department of Biochemistry and Microbiology, University of Victoria,
British Columbia, Canada.

Journal of bacteriology (UNITED STATES) Jun 1994, 176 (11) p3303-13,
ISSN 0021-9193 Journal Code: 2985120R

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

The polar flagellar filament of *Campylobacter coli* VC167 is composed of two highly related (98%) flagellin subunit proteins, FlaA and FlaB, whose antigenic specificities result from posttranslational modification. FlaA is the predominant flagellin species, and mutants expressing only FlaA form a full-length flagellar filament. Although the deduced M(r) of type 2 (T2) FlaA is 58,884 and the apparent M(r) by sodium dodecyl sulfate-polyacrylamide gel electrophoresis is 59,500, the solution weight-average M(r) by sedimentation analysis was 63,000. Circular dichroism studies in the presence or absence of 0.1% sodium dodecyl sulfate or 50% trifluorethanol showed that the secondary structure of T2 FlaA flagellin was altered, with alpha-helix structure being increased to 25% in the nonpolar environment. The molecule also contained 35 to 48% beta-sheet and 11 to 29% beta-turn structure. Mimeotope analysis of octapeptides representing the sequence of FlaA together with immunoelectron microscopy and enzyme-linked immunosorbent assay with a panel of antisera indicated that many residues in presumed linear epitopes were inaccessible or nonepitopic in the assembled filament, with the majority being in the N-terminal 337 residues of the 572-residue flagellin. Residues at the carboxy-terminal end of the T2 FlaA subunit also become inaccessible upon assembly. Digestion with trypsin, chymotrypsin, and endoproteinase Glu-C revealed a protease-resistant domain with an approximate M(r) of 18,700 between residues 193 and 375. Digestion with endoproteinase Arg-C and endoproteinase Lys-C allowed the mapping of a segment of surface-exposed FlaA sequence which contributes serospecificity to the VC167 T2 flagellar filament at residues between 421 and 480.

Tags: Support, Non-U.S. Gov't; Support, U.S. Gov't, Non-P.H.S.

Descriptors: *Antigens, Bacterial--immunology--IM; *Bacterial Proteins --immunology--IM; *Campylobacter coli--immunology--IM; *Flagella --immunology--IM; *Flagellin--immunology--IM; Amino Acid Sequence; Antigens, Bacterial--chemistry--CH; Antigens, Bacterial--genetics--GE; Bacterial Proteins--chemistry--CH; Bacterial Proteins--genetics--GE; Base Sequence; Campylobacter coli--chemistry--CH; Campylobacter coli--genetics --GE; Circular Dichroism; Enzyme-Linked Immunosorbent Assay; Epitopes; Flagella--chemistry--CH; Flagellin--chemistry--CH; Flagellin--genetics--GE ; Metalloendopeptidases--metabolism--ME; Microscopy, Immunoelectron; Molecular Sequence Data; Molecular Weight; Protein Structure, Secondary; Serine Endopeptidases--metabolism--ME; Serotyping; Spectrophotometry, Ultraviolet

CAS Registry No.: 0 (Antigens, Bacterial); 0 (Bacterial Proteins); 0 (Epitopes); 12777-81-0 (Flagellin); 133606-66-3 (flaA protein)
Enzyme No.: EC 3.4.21 (Serine Endopeptidases); EC 3.4.21.40 (submandibular proteinase A); EC 3.4.24 (Metalloendopeptidases); EC 3.4.24.20 (peptidyl-Lys metalloendopeptidase)
Gene Symbol: flaA
Record Date Created: 19940630

4/9/9 (Item 9 from file: 155)
DIALOG(R) File 155: MEDLINE(R)

07795270 93322323 PMID: 8331072

The *Campylobacter* sigma 54 *flaB* flagellin promoter is subject to environmental regulation.

Alm R A; Guerry P; Trust T J

Department of Biochemistry and Microbiology, University of Victoria, British Columbia, Canada.

Journal of bacteriology (UNITED STATES) Jul 1993, 175 (14) p4448-55,
ISSN 0021-9193 Journal Code: 2985120R

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

The complex flagellum of *Campylobacter coli* VC167 is encoded by two tandemly oriented flagellin genes which are transcribed as two discrete transcriptional units from two different classes of promoters. The *flaB* gene, which encodes the minor FlaB filament protein, is controlled by a sigma 54 promoter. A transcriptional fusion between a promoterless chloramphenicol acetyltransferase (CAT) reporter gene cartridge and *C. coli* VC167 DNA carrying *flaB* transcription and translation signals, including the typical position -13-to-(-)26 *flaB* sigma 54 consensus promoter sequence, was constructed. When carried on plasmid pRIC1013, the sigma 54-CAT fusion expressed chloramphenicol resistance in *Escherichia coli*, and CAT production was affected by the pH of the growth medium, the composition of the growth atmosphere, and the growth temperature, with production being significantly higher at 42 degrees C. A conjugative suicide vector, pRIC1028, containing the sigma 54-CAT fusion was constructed and used to recombine the *flaB*-CAT fusion back into the *C. coli* chromosome in the correct position with respect to the *flaA* gene and its transcription terminator. CAT production from the *flaB* sigma 54 promoter in the *C. coli* transconjugant VC167-T2/28-1 was shown to peak at mid-log phase and to be modulated by growth medium pH, growth temperature, and the concentration of certain inorganic salts and divalent cations in the growth medium. Under growth conditions which promoted elevated *flaB* sigma 54 promoter activity, a *flaA* *flaB*⁺ mutant of *C. coli* VC167 produced increased amounts of FlaB flagellar protein and displayed increased motility.

Tags: Support, Non-U.S. Gov't; Support, U.S. Gov't, Non-P.H.S.

Descriptors: *Bacterial Proteins--genetics--GE; *Campylobacter coli--genetics--GE; *Flagella--physiology--PH; *Flagellin--biosynthesis--BI; *Flagellin--genetics--GE; *Gene Expression Regulation, Bacterial; *Promoter Regions (Genetics); Base Sequence; *Campylobacter coli*--growth and development--GD; *Campylobacter coli*--physiology--PH; Cell Movement; Chloramphenicol O-Acetyltransferase--biosynthesis--BI; Chloramphenicol O-Acetyltransferase--genetics--GE; Chromosomes, Bacterial; Cloning, Molecular; Conjugation, Genetic; Culture Media; DNA, Bacterial--genetics--GE; DNA, Bacterial--isolation and purification--IP; *Escherichia coli*--genetics--GE; Gene Expression; Kinetics; Molecular Sequence Data; Oligodeoxyribonucleotides; Plasmids; Recombinant Fusion Proteins--biosynthesis--BI; Restriction Mapping

CAS Registry No.: 0 (Bacterial Proteins); 0 (Culture Media); 0 (DNA, Bacterial); 0 (Oligodeoxyribonucleotides); 0 (Plasmids); 0 (Recombinant Fusion Proteins); 12777-81-0 (Flagellin); 140470-87-7 (flaB protein)

Enzyme No.: EC 2.3.1.28 (Chloramphenicol O-Acetyltransferase)

Record Date Created: 19930813

4/9/10 (Item 10 from file: 155)
DIALOG(R) File 155: MEDLINE(R)

07733685 93259951 PMID: 8098328

Distribution and polymorphism of the flagellin genes from isolates of

Campylobacter coli and Campylobacter jejuni.

Alm R A; Guerry P; Trust T J

Department of Biochemistry and Microbiology, University of Victoria, British Columbia, Canada.

Journal of bacteriology (UNITED STATES) May 1993, 175 (10) p3051-7, ISSN 0021-9193 Journal Code: 2985120R

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

The complex flagellar filaments of the LIO8 serogroup member **Campylobacter coli** **VC167** are composed of two highly related subunit proteins encoded by the flaA and flaB genes which share 92% identity. Using oligonucleotide primers based on the known DNA sequence of both the flaA and flaB genes from *C. coli* **VC167** in the polymerase chain reaction, we have shown conservation of both fla genes among isolates within the LIO8 heat-labile serogroup by digestion of the amplified product with PstI and EcoRI restriction endonucleases. Amplification and subsequent restriction analysis of the flaA flagellin gene from **Campylobacter** isolates belonging to 13 different LIO serogroups further identified 10 unique polymorphic groups. Within most of the serogroups examined, isolates appeared to contain flaA genes with conserved primary structures. Only in serogroups LIO11 and LIO29 did independent isolates possess flagellin genes with different primary structures. Furthermore, by employing primers specific for the flaB gene of *C. coli* **VC167**, all serogroups examined contained a second fla gene corresponding to flaB. In all serogroups except the LIO5 and LIO6 isolates which were identical to each other, the polymorphic pattern of this flaB gene was identical to that of the corresponding flaA gene. These data indicate that the presence of a second highly homologous flagellin gene is widespread throughout **Campylobacter** isolates and that in most instances, the primary structure of the two fla genes is conserved within isolates belonging to the same heat-labile LIO serogroup. This may represent the presence of clonal evolutionary groups in **Campylobacter** spp.

Tags: Comparative Study; Support, Non-U.S. Gov't; Support, U.S. Gov't, Non-P.H.S.

Descriptors: *Bacterial Proteins--genetics--GE; *Campylobacter--genetics--GE; *Flagellin--genetics--GE; *Genes, Bacterial--genetics--GE; *Polymorphism, Restriction Fragment Length; Antigens, Bacterial--genetics--GE; Bacterial Typing Techniques; Base Sequence; Campylobacter--classification--CL; Campylobacter coli--classification--CL; Campylobacter coli--genetics--GE; Campylobacter jejuni--classification--CL; Campylobacter jejuni--genetics--GE; Molecular Sequence Data; Sequence Homology, Nucleic Acid; Serotyping

CAS Registry No.: 0 (Antigens, Bacterial); 0 (Bacterial Proteins); 12777-81-0 (Flagellin); 140470-87-7 (flaB protein)

Gene Symbol: flaB

Record Date Created: 19930611

4/9/11 (Item 11 from file: 155)
DIALOG(R) File 155: MEDLINE(R)

07694541 93217974 PMID: 8464049

Significance of duplicated flagellin genes in Campylobacter.

Alm R A; Guerry P; Trust T J

Department of Biochemistry and Microbiology, University of Victoria, British Columbia, Canada.

Journal of molecular biology (ENGLAND) Mar 20 1993, 230 (2) p359-63, ISSN 0022-2836 Journal Code: 2985088R

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

The complex flagellum of **Campylobacter coli** **VC167** contains two highly

related (98%) flagellin subunit proteins which are produced from two 92% homologous, tandemly orientated genes, flaA and flaB. Mutants expressing only flaA form a full-length flagellar filament that confers slightly less than wild-type motility to the bacterium. However, flagellin mutants expressing only flaB produce extremely short, truncated filaments, and are only slightly motile. We have shown that the presence of two essentially identical genes is advantageous, in that flaAflaB+ mutants become highly motile upon passage by an event which allows the production of a full length simple flagellar filament containing a single FlaA-FlaB chimeric flagellin protein. Furthermore, we have demonstrated that the reassortment of DNA that results in this chimeric protein can occur by two mechanisms: intragenomic recombination and transformation-mediated intergenomic recombination.

Tags: Comparative Study; Support, Non-U.S. Gov't; Support, U.S. Gov't, Non-P.H.S.

Descriptors: *Campylobacter coli--genetics--GE; *Flagellin--genetics--GE; *Genes, Structural, Bacterial; *Multigene Family; Amino Acid Sequence; Base Sequence; Macromolecular Systems; Molecular Sequence Data; Oligodeoxyribonucleotides; Restriction Mapping; Sequence Homology, Amino Acid

CAS Registry No.: 0 (Macromolecular Systems); 0 (Oligodeoxyribonucleotides); 12777-81-0 (Flagellin)

Gene Symbol: flaA; flaB

Record Date Created: 19930430

4/9/12 (Item 12 from file: 155)

DIALOG(R) File 155: MEDLINE(R)

07488954 93016725 PMID: 1400961

Specific detection of *Campylobacter jejuni* and *Campylobacter coli* by using polymerase chain reaction.

Oyofe B A; Thornton S A; Burr D H; Trust T J; Pavlovskis O R; Guerry P
Enteric Diseases Program, Naval Medical Research Institute, Bethesda,
Maryland 20889-5055.

Journal of clinical microbiology (UNITED STATES) Oct 1992, 30 (10)
p2613-9, ISSN 0095-1137 Journal Code: 7505564

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Development of a routine detection assay for *Campylobacter jejuni* and *Campylobacter coli* in clinical specimens was undertaken by using the polymerase chain reaction (PCR). An oligonucleotide primer pair from a conserved 5' region of the flaA gene of *C. coli* VC167 was used to amplify a 450-bp region by PCR. The primer pair specifically detected 4 strains of *C. coli* and 47 strains of *C. jejuni*; but it did not detect strains of *Campylobacter fetus*, *Campylobacter lari*, *Campylobacter upsaliensis*, *Campylobacter cryaerophila*, *Campylobacter butzleri*, *Campylobacter hyoilealis*, *Wolinella recta*, *Helicobacter pylori*, *Escherichia coli*, *Shigella* spp., *Salmonella* spp., *Vibrio cholerae*, *Citrobacter freundii*, or *Aeromonas* spp. By using a nonradioactively labeled probe internal to the PCR product, the assay could detect as little as 0.0062 pg of purified *C. coli* DNA, or the equivalent of four bacteria. In stools seeded with *C. coli* cells, the probe could detect between 30 and 60 bacteria per PCR assay. The assay was also successfully used to detect *C. coli* in rectal swab specimens from experimentally infected rabbits and *C. jejuni* in human stool samples.

Tags: Animal; Female; Human; Support, Non-U.S. Gov't; Support, U.S. Gov't, Non-P.H.S.

Descriptors: *Campylobacter coli--isolation and purification--IP; *Campylobacter jejuni--isolation and purification--IP; *Flagellin--genetics--GE; *Genes, Bacterial--genetics--GE; *Polymerase Chain Reaction; Base Sequence; Campylobacter Infections--microbiology--MI; Campylobacter coli--genetics--GE; Campylobacter jejuni--genetics--GE; DNA, Single-Stranded; Feces--microbiology--MI; Molecular Sequence Data; Rabbits; Sensitivity and Specificity

CAS Registry No.: 0 (DNA, Single-Stranded); 12777-81-0 (Flagellin)
Gene Symbol: flaA; flaB
Record Date Created: 19921110

4/9/13 (Item 13 from file: 155)
DIALOG(R) File 155: MEDLINE(R)

07392364 92325005 PMID: 1624417

Variation in antigenicity and molecular weight of *Campylobacter coli* VC167 flagellin in different genetic backgrounds.

Alm R A; Guerry P; Power M E; Trust T J

Department of Biochemistry and Microbiology, University of Victoria, British Columbia.

Journal of bacteriology (UNITED STATES) Jul 1992, 174 (13) p4230-8,
ISSN 0021-9193 Journal Code: 2985120R

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Campylobacter coli* VC167** has been shown to undergo a reversible flagellar antigenic variation between antigenic type 1 (T1) and antigenic type 2 (T2). VC167 contains two flagellin genes, and the products of both genes are incorporated into a complex flagellar filament in both antigenic types. Although there are only minor amino acid changes in the flagellins expressed by T1 and T2 cells, the two antigenic types of flagellins can be distinguished by differences in apparent M(r) on sodium dodecyl sulfate-polyacrylamide gels and by immunoreactivity with T1-specific (LAH1) or T2-specific (LAH2) antiserum. The isolation of stable variants of T1 and T2 has allowed for the transfer via natural transformation of the flagellin structural genes from the T1 background into the T2 background and from the T2 background into the T1 background. In addition, the flagellin genes from VC167 T1 and T2 have been transferred into strains of ***Campylobacter jejuni. The results indicate that the observed antigenic variations of VC167 flagellins are dependent on the host genetic background and independent of the primary amino acid sequence. These data provide evidence that posttranslational modifications are responsible for the antigenic variation seen in VC167 flagellins.

Tags: Support, Non-U.S. Gov't; Support, U.S. Gov't, Non-P.H.S.

Descriptors: *Antigenic Variation; *Campylobacter coli--genetics--GE; *Flagellin--genetics--GE; *Genes, Structural, Bacterial; Base Sequence; Blotting, Southern; Campylobacter coli--immunology--IM; Campylobacter coli--ultrastructure--UL; Conjugation, Genetic; DNA, Bacterial--genetics--GE; DNA, Bacterial--isolation and purification--IP; Enzyme-Linked Immunosorbent Assay; Escherichia coli--genetics--GE; Flagella--physiology--PH; Flagella--ultrastructure--UL; Flagellin--immunology--IM; Microscopy, Immunoelectron; Molecular Sequence Data; Mutagenesis, Site-Directed; Oligodeoxyribonucleotides; Restriction Mapping; Transformation, Bacterial

CAS Registry No.: 0 (DNA, Bacterial); 0 (Oligodeoxyribonucleotides);

12777-81-0 (Flagellin)

Gene Symbol: flaA; flaB

Record Date Created: 19920807

4/9/14 (Item 14 from file: 155)
DIALOG(R) File 155: MEDLINE(R)

07187757 92129509 PMID: 1774247

Analysis of the role of flagella in the heat-labile Lior serotyping scheme of thermophilic *Campylobacters* by mutant allele exchange.

Alm R A; Guerry P; Power M E; Lior H; Trust T J

Department of Biochemistry and Microbiology, University of Victoria, British Columbia.

Journal of clinical microbiology (UNITED STATES) Nov 1991, 29 (11) p2438-45, ISSN 0095-1137 Journal Code: 7505564

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Flagellin mutations originally constructed in *Campylobacter coli* VC167 (serotype LIO8) by a gene replacement mutagenesis technique (P. Guerry, S. M. Logan, S. Thornton, and T. J. Trust, J. Bacteriol. 172:1853-1860, 1990) were moved from the original host into *Campylobacter* strains of a number of other Lior serogroups by a natural transformation procedure. This is the first report of the use of this transformation method to transfer a mutated locus among *Campylobacter* strains. Flagellin mutants were constructed in a number of heat-labile LIO serotypes and were serotyped and analyzed by immunolectron microscopy with LIO typing antisera. In six cases, isogenic nonflagellated mutants were able to be serotyped in the same serogroup as their parent, and immunogold electron microscopy confirmed that antibodies in the typing antisera bound to components on the surface of both parent and mutant cells. However, in only one case, a strain belonging to serogroup LIO4, was a nonflagellated mutant untypeable, and immunogold electron microscopy showed that antibodies bound to the flagella filament of the parent but not to the cell surface. Furthermore, after introduction and expression as a flagellar filament of a LIO8 flagellin gene in this mutant, the strain could not be serotyped. These results indicate that a nonflagellar antigen is often the serodeterminant in the heat-labile Lior serotyping scheme.

Tags: Support, Non-U.S. Gov't; Support, U.S. Gov't, Non-P.H.S.

Descriptors: *Campylobacter coli--classification--CL; *Campylobacter coli--ultrastructure--UL; *Campylobacter jejuni--classification--CL; *Campylobacter jejuni--ultrastructure--UL; *Flagella--ultrastructure--UL; Alleles; Campylobacter coli--genetics--GE; Campylobacter jejuni--genetics--GE; Flagella--physiology--PH; Flagellin--genetics--GE; Genes, Bacterial; Heat; Mutation; Serotyping--methods--MT

CAS Registry No.: 12777-81-0 (Flagellin)

Gene Symbol: flaA; flaB

Record Date Created: 19920305

4/9/17 (Item 17 from file: 155)

DIALOG(R) File 155: MEDLINE(R)

06617454 90316700 PMID: 2370114

Polynucleotide sequence relationships among flagellin genes of *Campylobacter jejuni* and *Campylobacter coli*.

Thornton S A; Logan S M; Trust T J; Guerry P

Infectious Diseases Department, Naval Medical Research Institute, Bethesda, Maryland 20814.

Infection and immunity (UNITED STATES) Aug 1990, 58 (8) p2686-9,
ISSN 0019-9567 Journal Code: 0246127

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

DNA probes that encode a complete flagellin gene and various internal regions of the *Campylobacter coli* VC167 flagellin genes were hybridized to 30 strains of *C. coli* or *C. jejuni* from 20 different Lior serogroups. The results indicated a high overall degree of homology among all of the strains examined. Although the most variable regions occurred within the middle of the gene, significant DNA homology was observed among many serogroups in this region of the molecule.

Tags: Comparative Study; Support, Non-U.S. Gov't; Support, U.S. Gov't, Non-P.H.S.

Descriptors: *Bacterial Proteins--genetics--GE; *Campylobacter--genetics--GE; *Campylobacter fetus--genetics--GE; *Flagellin--genetics--GE; *Genes, Bacterial; Blotting, Southern; Campylobacter--classification--CL; Campylobacter fetus--classification--CL; DNA Probes; DNA, Bacterial; Nucleic Acid Hybridization; Sequence Homology, Nucleic Acid; Serotyping

CAS Registry No.: 0 (Bacterial Proteins); 0 (DNA Probes); 0 (DNA,

Bacterial); 12777-81-0 (Flagellin)
Record Date Created: 19900821

4/9/18 (Item 18 from file: 155)
DIALOG(R) File 155: MEDLINE(R)

06498291 90202702 PMID: 2318805

Genomic organization and expression of *Campylobacter* flagellin genes.
Guerry P; Logan S M; Thornton S; Trust T J
Infectious Diseases Department, Naval Medical Research Institute, Bethesda, Maryland 20814.
Journal of bacteriology (UNITED STATES) Apr 1990, 172 (4) p1853-60,
ISSN 0021-9193 Journal Code: 2985120R

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Campylobacter coli VC167, which undergoes an antigenic flagellar variation, contains two full-length flagellin genes, flaA and flaB, that are located adjacent to one another in a tandem orientation and are 91.5% homologous. The gene product of flaB, which has an Mr of 58,946, has 93% sequence homology to the gene product of flaA, which has an Mr of 58,916 (S. M. Logan, T. J. Trust, and P. Guerry, J. Bacteriol. 171:3031-3038, 1989). Mutational analyses and primer extension experiments indicated that the two genes are transcribed under the control of distinct promoters but that they are expressed concomitantly in the same cell, regardless of the antigenic phase of flagella being produced. The flaA gene, which was expressed at higher levels than the flaB gene in both phases, was transcribed from a typical sigma 28-type promoter, whereas the flaB promoter was unusual. A mutant producing only the flaB gene product did not synthesize a flagellar filament and was nonmotile. Southern blot analysis indicated that flagellar antigenic variation involves a rearrangement of flagellin sequence information rather than the alternate expression of the two distinct genes.

Tags: Comparative Study; Support, Non-U.S. Gov't; Support, U.S. Gov't, Non-P.H.S.

Descriptors: *Bacterial Proteins--genetics--GE; *Campylobacter--genetics--GE; *Flagellin--genetics--GE; *Genes, Bacterial; Amino Acid Sequence; Base Sequence; Blotting, Western; Cloning, Molecular; DNA, Bacterial--genetics--GE; Molecular Sequence Data; Mutation; Nucleic Acid Hybridization; Plasmids; Promoter Regions (Genetics); Restriction Mapping; Sequence Homology, Nucleic Acid; Variation (Genetics)

Molecular Sequence Databank No.: GENBANK/M35141

CAS Registry No.: 0 (Bacterial Proteins); 0 (DNA, Bacterial); 0 (Plasmids); 12777-81-0 (Flagellin)

Record Date Created: 19900502

4/9/19 (Item 19 from file: 155)
DIALOG(R) File 155: MEDLINE(R)

06223240 89307586 PMID: 2744863

In vivo antigenic variation of *Campylobacter* flagellin.
Logan S M; Guerry P; Rollins D M; Burr D H; Trust T J
Department of Biochemistry and Microbiology, University of Victoria, British Columbia, Canada.

Infection and immunity (UNITED STATES) Aug 1989, 57 (8) p2583-5,
ISSN 0019-9567 Journal Code: 0246127

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Campylobacter coli VC167 cells producing either antigenic phase 1 (P1) or phase 2 (P2) flagellins (as determined by characteristic protein

and DNA patterns) were used to infect rabbits by the removable intestinal tie-adult rabbit diarrhea (RITARD) procedure. Rabbits infected with P2 cells shed predominantly P2 cells throughout the infection; in rabbits infected with P1 cells, a transition of fecal isolates from P1 to P2 was observed.

Tags: Animal; Support, Non-U.S. Gov't; Support, U.S. Gov't, Non-P.H.S.

Descriptors: *Antigenic Variation; *Antigens, Bacterial--isolation and purification--IP; *Bacterial Proteins--isolation and purification--IP; *Campylobacter--immunology--IM; *Flagellin--isolation and purification--IP; Antigens, Bacterial--genetics--GE; DNA, Bacterial --isolation and purification--IP; Diarrhea--microbiology--MI; Flagellin--genetics--GE; Rabbits

CAS Registry No.: 0 (Antigens, Bacterial); 0 (Bacterial Proteins); 0 (DNA, Bacterial); 12777-81-0 (Flagellin)

Record Date Created: 19890818

4/9/20 (Item 20 from file: 155)

DIALOG(R) File 155: MEDLINE(R)

06170100 89255058 PMID: 2722741

Evidence for posttranslational modification and gene duplication of *Campylobacter* flagellin.

Logan S M; Trust T J; Guerry P

Department of Biochemistry and Microbiology, University of Victoria, British Columbia.

Journal of bacteriology (UNITED STATES) Jun 1989, 171 (6) p3031-8, ISSN 0021-9193 Journal Code: 2985120R

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

A gene encoding a flagellin protein of *Campylobacter* coli **VC167** has been cloned and sequenced. The gene was identified in a pBR322 library by hybridization to a synthetic oligonucleotide probe corresponding to amino acids 4 to 9 of the N-terminal sequence obtained by direct chemical analysis (S. M. Logan, L. A. Harris, and T. J. Trust, J. Bacteriol. 169:5072-5077, 1987). The DNA was sequenced and shown to contain an open reading frame encoding a protein with a molecular weight of 58,945 and a length of 572 amino acids. The deduced amino acid sequence was identical to the published N-terminal amino acid sequence of **VC167** flagellin and to four internal regions whose partial sequences were obtained by direct chemical analysis of two tryptic and two cyanogen bromide peptides of VC167 flagellin. The *C. coli* flagellin protein contains posttranslationally modified serine residues, most of which occur within a region containing two 9-amino-acid repeating peptides separated by 34 unique amino acids. Comparisons with the sequences of flagellins from other bacterial species revealed conserved residues at the amino- and carboxy-terminal regions. Hybridization data suggest the presence of a second flagellin copy located adjacent to the first on the VC167 chromosome.

Tags: Support, Non-U.S. Gov't; Support, U.S. Gov't, Non-P.H.S.

Descriptors: *Bacterial Proteins--genetics--GE; *Campylobacter--genetics--GE; *Flagellin--genetics--GE; Amino Acid Sequence; Base Sequence; Blotting, Southern; Cloning, Molecular; DNA, Bacterial--genetics--GE; Flagellin--immunology--IM; Genes, Bacterial; Molecular Sequence Data; Multigene Family; Protein Processing, Post-Translational

Molecular Sequence Databank No.: GENBANK/M26945

CAS Registry No.: 0 (Bacterial Proteins); 0 (DNA, Bacterial); 12777-81-0 (Flagellin)

Record Date Created: 19890705

4/9/21 (Item 21 from file: 155)

DIALOG(R) File 155: MEDLINE(R)

05669263 88086888 PMID: 2826396